Frantz Depaulis

Phylogenetic methods to detect selection , an application on hepatitis C virus: overcoming recombination

I shall review phylogenetic methods to detect selection, PAML and HYPHY programs and corresponding user friendly servers: selecton and datamonkey. I will present an application on hepatitis C virus within patient evolution, with envelope sequences over two time samples (n=89). I will focus in particular on how to account for recombination, corresponding published strategies and associated caveats and will propose a more conservative alternative procedure. Results show evidence of recombination of positive selection on a few codons, with the two time samples being significantly differentiated.

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Evolution of virulence: an empirical test of the trade-off hypothesis on a plant-virus

An adaptive hypothesis proposed to explain the evolution of virulence in parasites is known as the trade-off hypothesis. This hypothesis states that an increase in parasite transmission is linked to an increase in the mortality rate of the host (virulence). A positive correlation between transmission and virulence is then predicted in hosts into which the parasite evolved. Surprisingly, no prediction has ever been proposed for parasites infecting a new host species and few studies tested the correlations between virulence (or transmission rates) in the native and new host. In order to fill these gaps, we infected Brassica rapa (native host) and Arabidopsis thaliana (new host) plants with nine natural population of Cauliflower mosaic virus (CaMV) and then estimated transmission rate and virulence. As predicted by the trade-off hypothesis, we observed a positive correlation between the rate of transmission and the virulence of CaMV on the native host. Interestingly, we also observe such positive correlation in the new host. Moreover, neither virulence nor transmission rates in the two hosts were correlated. It seems thus impossible to predict the levels of these traits in a new host from its evaluation on the native host. However, our results allow us to predict that, even on a new host, evolution of both traits will be linked.

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Distribution and conservation of Banana Streak Virus (BSV) within banana Musa balbisiana genome : what impact on host and virus evolution?

The nuclear genome of several plants is invaded by numerous viral sequences. These integrations correspond to accidental events mainly resulting from illegitimate recombination of DNA viruses belonging to the family Caulimoviridae with plant DNA whereas integration into the host genome is not required for viral replication. These integrations are for the most part defective as a result of pseudogenisation driven by the host genome evolution. Conversely, some other integrations named infectious, could release a functional viral genome following activating stresses.
Our aim is to study the integration context of such infectious integrants for Banana streak virus among the diversity of the banana B genome in order to retrace the evolutionary BSV story and understand their impact on host and virus evolution in terms of cost/benefit. To answer this question, we propose to characterize infectious integrants (eBSV) among a representative sampling of Musa balbisiana diversity and to hypothesize a contribution of eBSV towards plant virus resistance through an RNA interfering mechanism versus a maintain of the virus through interspecific crosses.

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